



10

SEQUENCE LISTING

<110> Andersen, Carsten
Borchert, Torben Vedel
Nielsen, Bjarne Ronfeldt

<120> Amylase Variants

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<170> PatentIn version 3.1

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aac	tta	aag	agt	aaa	ggg	ata	aca	gct	gta	tgg	atc	cca	cct	gca	tgg	144
Asn	Leu	Lys	Ser	Lys	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Trp	
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aca	cgc	aac	cag	cta	cag	gct	gcg	gtg	acc	tct	tta	aaa	aat	aac	ggc	288
Thr	Arg	Asn	Gln	Leu	Gln	Ala	Ala	Val	Thr	Ser	Leu	Lys	Asn	Asn	Gly	
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att	cag	gta	tat	ggt	gat	gtc	gtc	atg	aat	cat	aaa	ggt	gga	gca	gat	336
Ile	Gln	Val	Tyr	Gly	Asp	Val	Val	Met	Asn	His	Lys	Gly	Gly	Ala	Asp	
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ggt	acg	gaa	att	gta	aat	gcg	gta	gaa	gtg	aat	cgg	agc	aac	cga	aac	384
Gly	Thr	Glu	Ile	Val	Asn	Ala	Val	Glu	Val	Asn	Arg	Ser	Asn	Arg	Asn	
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aca gag aat ggc aac tat gac tat ctt atg tat gca gac gtg gat atg Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met 195 200 205	624
gat cac cca gaa gta ata cat gaa ctt aga aac tgg gga gtg tgg tat Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr 210 215 220	672
acg aat aca ctg aac ctt gat gga ttt aga ata gat gca gtg aaa cat Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His 225 230 235 240	720
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Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr	
385 390 395 400	
cag cat gat tac ttt gat cat cat gat att atc ggt tgg aca aga gag	1248
Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu	
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Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp	
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Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr	

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55

60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
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Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
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Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
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Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
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Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
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Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
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His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
165 170 175

Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
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195 200 205

Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr
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Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
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Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
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Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
 305 310 315 320

His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
 325 330 335

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Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
 355 360 365

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 370 375 380

Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
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Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
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Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly
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Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
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aat cta aga aat aga ggt ata acc gct att tgg att ccg cct gcc tgg	144
Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp	
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Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr	
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caa cat gat tat ttt gac cat cat aat ata atc gga tgg aca cgt gaa Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu 405 410 415	1248
gga aat acc acg cat ccc aat tca gga ctt gcg act atc atg tcg gat	1296

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Asn	Ala	Asp	Gly	Trp	Ala	Asn	Phe	Ser	Val	Asn	Gly	Gly	Ser	Val	Ser		
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Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr
 145 150 155 160

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 165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp
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Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
 195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr
 210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
 225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala
 245 250 255

Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
 260 265 270

Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
 275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
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Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys
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His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
 325 330 335

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Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
 355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala
 370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr
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Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
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Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
 420 425 430

Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly
 435 440 445

Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile
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Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr	
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aaa gct caa tat ctt caa gcc att caa gcc gcc cac gcc gct gga atg	288
Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala His Ala Ala Gly Met	
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Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly	
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Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln	
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Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe	
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Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His	
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Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr	
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Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu	
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Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln Thr Gly	
245 250 255	
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Phe	Ile	Leu	Thr	Arg	Gln	Glu	Gly	Tyr	Pro	Cys	Val	Phe	Tyr	Gly	Asp		
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tat	tat	ggc	att	cca	caa	tat	aac	att	cct	tcg	ctg	aaa	agc	aaa	atc		1152
Tyr	Tyr	Gly	Ile	Pro	Gln	Tyr	Asn	Ile	Pro	Ser	Leu	Lys	Ser	Lys	Ile		
	370				375				380								
gat	ccg	ctc	ctc	atc	gcg	cgc	agg	gat	tat	gct	tac	gga	acg	caa	cat		1200
Asp	Pro	Leu	Leu	Ile	Ala	Arg	Arg	Asp	Tyr	Ala	Tyr	Gly	Thr	Gln	His		
385				390				395						400			
gat	tat	ctt	gat	cac	tcc	gac	atc	atc	ggg	tgg	aca	agg	gaa	ggg	ggc		1248
Asp	Tyr	Leu	Asp	His	Ser	Asp	Ile	Ile	Gly	Trp	Thr	Arg	Glu	Gly	Gly		
				405				410					415				
act	gaa	aaa	cca	gga	tcc	gga	ctg	gcc	gca	ctg	atc	acc	gat	ggg	ccg		1296
Thr	Glu	Lys	Pro	Gly	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro		
		420					425					430					
gga	gga	agc	aaa	tgg	atg	tac	gtt	ggc	aaa	caa	cac	gct	gga	aaa	gtg		1344
Gly	Gly	Ser	Lys	Trp	Met	Tyr	Val	Gly	Lys	Gln	His	Ala	Gly	Lys	Val		
		435				440						445					
ttc	tat	gac	ctt	acc	ggc	aac	cgg	agt	gac	acc	gtc	acc	atc	aac	agt		1392
Phe	Tyr	Asp	Leu	Thr	Gly	Asn	Arg	Ser	Asp	Thr	Val	Thr	Ile	Asn	Ser		
	450				455						460						
gat	gga	tgg	ggg	gaa	ttc	aaa	gtc	aat	ggc	ggt	tcg	gtt	tcg	gtt	tgg		1440
Asp	Gly	Trp	Gly	Glu	Phe	Lys	Val	Asn	Gly	Gly	Ser	Val	Ser	Val	Trp		
465				470				475						480			
gtt	cct	aga	aaa	acg	acc	gtt	tct	acc	atc	gct	cgg	ccg	atc	aca	acc		1488
Val	Pro	Arg	Lys	Thr	Thr	Val	Ser	Thr	Ile	Ala	Arg	Pro	Ile	Thr	Thr		

	485		490		495	
cga ccg tgg act ggt gaa ttc gtc cgt tgg acc gaa cca cgg ttg gtg						1536
Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val						
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gca tgg cct tga						1548
Ala Trp Pro						
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Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys						
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Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp						
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Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr						
65	70		75		80	
Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met						
	85		90		95	
Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly						
	100		105		110	
Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln						
	115		120		125	
Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe						
	130		135		140	
Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His						
145	150		155		160	

Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr
 165 170 175

Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu
 180 185 190

Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His
 195 200 205

Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr Val Asn
 210 215 220

Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys
 225 230 235 240

Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln Thr Gly
 245 250 255

Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys
 260 265 270

Leu His Asn Tyr Ile Thr Lys Thr Asp Gly Thr Met Ser Leu Phe Asp
 275 280 285

Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Ala
 290 295 300

Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro
 305 310 315 320

Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln
 325 330 335

Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala
 340 345 350

Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp
 355 360 365

Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile
 370 375 380

Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His
 385 390 395 400

Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Gly
 405 410 415

Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430

Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val
 435 440 445

Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser
 450 455 460

Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp
 465 470 475 480

Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr Thr
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Ala Trp Pro
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 <213> Bacillus licheniformis

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 <222> (421)..(1872)
 <223> Termamyl

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 agattattaa aaagctgaaa gcaaaaaggct atcaattggt aactgtatct cagcttgaag 180
 aagtgaagaa gcagagaggc tattgaataa atgagtagaa gcgccatatc ggcgcttttc 240
 ttttggaaga aaatataggg aaaatggtac ttgttaaaaa ttcggaatat ttatacaaca 300

tcatatgttt	cacattgaaa	ggggaggaga	atcatgaaac	aacaaaaacg	gctttacgcc	360
cgattgctga	cgctgttatt	tgcgctcatc	ttcttgctgc	ctcattctgc	agcagcggcg	420
gca aat ctt aat ggg acg ctg atg cag tat ttt gaa tgg tac atg ccc	468					
Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro						
1 5 10 15						
aat gac ggc caa cat tgg agg cgt ttg caa aac gac tcg gca tat ttg	516					
Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu						
20 25 30						
gct gaa cac ggt att act gcc gtc tgg att ccc ccg gca tat aag gga	564					
Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly						
35 40 45						
acg agc caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta	612					
Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu						
50 55 60						
ggg gag ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa	660					
Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys						
65 70 75 80						
gga gag ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac	708					
Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn						
85 90 95						
gtt tac ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc	756					
Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr						
100 105 110						
gaa gat gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta	804					
Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val						
115 120 125						
att tca gga gaa cac cta att aaa gcc tgg aca cat ttt cat ttt ccg	852					
Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro						
130 135 140						
ggg cgc ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt	900					
Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe						
145 150 155 160						
gac gga acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag	948					
Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys						
165 170 175						
ttt caa gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac	996					
Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn						
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tat gat tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc	1044					
Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val						
195 200 205						

gca gca gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln 210 215 220	1092
ttg gac ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe 225 230 235 240	1140
ttg cgg gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met 245 250 255	1188
ttt acg gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn 260 265 270	1236
tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu 275 280 285	1284
cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met 290 295 300	1332
agg aaa ttg ctg aac ggt acg gtc gtt tcc aag cat ccg ttg aaa tcg Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser 305 310 315 320	1380
gtt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu 325 330 335	1428
tcg act gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu 340 345 350	1476
aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly 355 360 365	1524
acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile 370 375 380	1572
gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His 385 390 395 400	1620
gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp 405 410 415	1668
agc tcg gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro 420 425 430	1716
ggc ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca	1764

Gly	Gly	Ala	Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr		
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tgg	cat	gac	att	acc	gga	aac	cgt	tcg	gag	ccg	gtt	gtc	atc	aat	tcg	1812	
Trp	His	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser		
		450				455					460						
gaa	ggc	tgg	gga	gag	ttt	cac	gta	aac	ggc	ggg	tcg	gtt	tca	att	tat	1860	
Glu	Gly	Trp	Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr		
465					470				475					480			
gtt	caa	aga	tag	aagagcagag	aggacggatt	tcctgaagga	aatccgtttt									1912	
Val	Gln	Arg															
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1			5					10						15			
Asn	Asp	Gly	Gln	His	Trp	Arg	Arg	Leu	Gln	Asn	Asp	Ser	Ala	Tyr	Leu		
		20						25					30				
Ala	Glu	His	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly		
		35					40					45					
Thr	Ser	Gln	Ala	Asp	Val	Gly	Tyr	Gly	Ala	Tyr	Asp	Leu	Tyr	Asp	Leu		
	50					55					60						
Gly	Glu	Phe	His	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys		
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Gly	Glu	Leu	Gln	Ser	Ala	Ile	Lys	Ser	Leu	His	Ser	Arg	Asp	Ile	Asn		
			85					90						95			
Val	Tyr	Gly	Asp	Val	Val	Ile	Asn	His	Lys	Gly	Gly	Ala	Asp	Ala	Thr		
		100					105						110				
Glu	Asp	Val	Thr	Ala	Val	Glu	Val	Asp	Pro	Ala	Asp	Arg	Asn	Arg	Val		
		115					120					125					

Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro
 130 135 140

Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
 145 150 155 160

Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
 165 170 175

Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
 180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
 195 200 205

Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
 210 215 220

Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
 225 230 235 240

Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
 245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
 260 265 270

Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
 275 280 285

His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
 290 295 300

Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
 305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
 340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly

355

360

365

Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
 370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
 385 390 395 400

Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
 405 410 415

Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430

Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
 435 440 445

Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
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Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
 465 470 475 480

Val Gln Arg

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 <213> Bacillus amyloliquefaciens

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 <222> (343)..(1794)
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acgctgttat ttgtcagttt gccgattaca aaaacatcag cc gta aat ggc acg	354
Val Asn Gly Thr	
1	
ctg atg cag tat ttt gaa tgg tat acg ccg aac gac ggc cag cat tgg	402
Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp Gly Gln His Trp	
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aaa cga ttg cag aat gat gcg gaa cat tta tcg gat atc gga atc act	450
Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp Ile Gly Ile Thr	
25 30 35	
gcc gtc tgg att cct ccc gca tac aaa gga ttg agc caa tcc gat aac	498
Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser Gln Ser Asp Asn	
40 45 50	
gga tac gga cct tat gat ttg tat gat tta gga gaa ttc cag caa aaa	546
Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Gln Gln Lys	
55 60 65	
ggg acg gtc aga acg aaa tac ggc aca aaa tca gag ctt caa gat gcg	594
Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu Leu Gln Asp Ala	
70 75 80	
atc ggc tca ctg cat tcc cgg aac gtc caa gta tac gga gat gtg gtt	642
Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr Gly Asp Val Val	
85 90 95 100	
ttg aat cat aag gct ggt gct gat gca aca gaa gat gta act gcc gtc	690
Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp Val Thr Ala Val	
105 110 115	
gaa gtc aat ccg gcc aat aga aat cag gaa act tcg gag gaa tat caa	738
Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser Glu Glu Tyr Gln	
120 125 130	
atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt gga aac acg tac	786
Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg Gly Asn Thr Tyr	
135 140 145	
agt gat ttt aaa tgg cat tgg tat cat ttc gac gga gcg gac tgg gat	834
Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Ala Asp Trp Asp	
150 155 160	
gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt ggg gaa gga aaa	882
Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg Gly Glu Gly Lys	
165 170 175 180	
gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac tat gac tat tta	930
Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn Tyr Asp Tyr Leu	
185 190 195	
atg tat gct gat gtt gac tac gac cac cct gat gtc gtg gca gag aca	978
Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val Val Ala Glu Thr	
200 205 210	
aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca tta gac ggc ttc	1026

Lys	Lys	Trp	Gly	Ile	Trp	Tyr	Ala	Asn	Glu	Leu	Ser	Leu	Asp	Gly	Phe		
		215					220					225					
cgt	att	gat	gcc	gcc	aaa	cat	att	aaa	ttt	tca	ttt	ctg	cgt	gat	tgg	1074	
Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	Ser	Phe	Leu	Arg	Asp	Trp		
	230					235					240						
gtt	cag	gcg	gtc	aga	cag	gcg	acg	gga	aaa	gaa	atg	ttt	acg	gtt	gcg	1122	
Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	Glu	Met	Phe	Thr	Val	Ala		
245					250					255					260		
gag	tat	tgg	cag	aat	aat	gcc	ggg	aaa	ctc	gaa	aac	tac	ttg	aat	aaa	1170	
Glu	Tyr	Trp	Gln	Asn	Asn	Ala	Gly	Lys	Leu	Glu	Asn	Tyr	Leu	Asn	Lys		
			265					270						275			
aca	agc	ttt	aat	caa	tcc	gtg	ttt	gat	gtt	ccg	ctt	cat	ttc	aat	tta	1218	
Thr	Ser	Phe	Asn	Gln	Ser	Val	Phe	Asp	Val	Pro	Leu	His	Phe	Asn	Leu		
		280						285					290				
cag	gcg	gct	tcc	tca	caa	gga	ggc	gga	tat	gat	atg	agg	cgt	ttg	ctg	1266	
Gln	Ala	Ala	Ser	Ser	Gln	Gly	Gly	Gly	Tyr	Asp	Met	Arg	Arg	Leu	Leu		
	295					300						305					
gac	ggc	acc	gtt	gtg	tcc	agg	cat	ccg	gaa	aag	gcg	gtt	aca	ttt	gtt	1314	
Asp	Gly	Thr	Val	Val	Ser	Arg	His	Pro	Glu	Lys	Ala	Val	Thr	Phe	Val		
	310				315						320						
gaa	aat	cat	gac	aca	cag	ccg	gga	cag	tca	ttg	gaa	tcg	aca	gtc	caa	1362	
Glu	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu	Ser	Thr	Val	Gln		
325					330					335					340		
act	tgg	ttt	aaa	ccg	ctt	gca	tac	gcc	ttt	att	ttg	aca	aga	gaa	tcc	1410	
Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Arg	Glu	Ser		
			345					350						355			
ggc	tat	cct	cag	gtg	ttc	tat	ggg	gat	atg	tac	ggg	aca	aaa	ggg	aca	1458	
Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly	Thr	Lys	Gly	Thr		
		360					365					370					
tcg	cca	aag	gaa	att	ccc	tca	ctg	aaa	gat	aat	ata	gag	ccg	att	tta	1506	
Ser	Pro	Lys	Glu	Ile	Pro	Ser	Leu	Lys	Asp	Asn	Ile	Glu	Pro	Ile	Leu		
	375					380						385					
aaa	gcg	cgt	aag	gag	tac	gca	tac	ggg	ccc	cag	cac	gat	tat	att	gac	1554	
Lys	Ala	Arg	Lys	Glu	Tyr	Ala	Tyr	Gly	Pro	Gln	His	Asp	Tyr	Ile	Asp		
	390					395				400							
cac	ccg	gat	gtg	atc	gga	tgg	acg	agg	gaa	ggc	gac	agc	tcc	gcc	gcc	1602	
His	Pro	Asp	Val	Ile	Gly	Trp	Thr	Arg	Glu	Gly	Asp	Ser	Ser	Ala	Ala		
405					410					415					420		
aaa	tca	ggc	ttg	gcc	gct	tta	atc	acg	gac	gga	ccc	ggc	gga	tca	aag	1650	
Lys	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro	Gly	Gly	Ser	Lys		
			425					430					435				
cgg	atg	tat	gcc	ggc	ctg	aaa	aat	gcc	ggc	gag	aca	tgg	tat	gac	ata	1698	
Arg	Met	Tyr	Ala	Gly	Leu	Lys	Asn	Ala	Gly	Glu	Thr	Trp	Tyr	Asp	Ile		

440	445	450	
acg ggc aac cgt tca gat act gta aaa atc gga tct gac ggc tgg gga			1746
Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser Asp Gly Trp Gly			
455	460	465	
gag ttt cat gta aac gat ggg tcc gtc tcc att tat gtt cag aaa taa			1794
Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr Val Gln Lys			
470	475	480	
ggtaataaaaa aaacacctcc aagctgagtg cgggtatcag cttggaggtg cgttttat			1854
ttcagccgta tgacaagggtc ggcacaggt gtgacaaata cggtatgctg gctgtcatag			1914
gtgacaaatc cgggttttgc gccgtttggc tttttcacat gtctgatttt tgtataatca			1974
acaggcacgg agccggaatc tttcgccttg gaaaaataag cggcgatcgt agctgcttcc			2034
aatatggatt gttcatcggg atcgctgctt ttaatcacaa cgtgggatcc			2084
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<212>	PRT		
<213>	Bacillus amyloliquefaciens		
<400>	10		
Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp			
1	5	10	15
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp			
20	25	30	
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser			
35	40	45	
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu			
50	55	60	
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu			
65	70	75	80
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr			
85	90	95	
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp			
100	105	110	
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser			

115		120		125											
Glu	Glu	Tyr	Gln	Ile	Lys	Ala	Trp	Thr	Asp	Phe	Arg	Phe	Pro	Gly	Arg
130						135					140				
Gly	Asn	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly
145					150					155					160
Ala	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Ile	Ser	Arg	Ile	Phe	Lys	Phe	Arg
				165					170					175	
Gly	Glu	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Ser	Glu	Asn	Gly	Asn
			180					185					190		
Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Val	Asp	Tyr	Asp	His	Pro	Asp	Val
	195						200					205			
Val	Ala	Glu	Thr	Lys	Lys	Trp	Gly	Ile	Trp	Tyr	Ala	Asn	Glu	Leu	Ser
	210					215					220				
Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	Ser	Phe
225					230					235					240
Leu	Arg	Asp	Trp	Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	Glu	Met
				245					250					255	
Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asn	Ala	Gly	Lys	Leu	Glu	Asn
		260						265					270		
Tyr	Leu	Asn	Lys	Thr	Ser	Phe	Asn	Gln	Ser	Val	Phe	Asp	Val	Pro	Leu
	275						280					285			
His	Phe	Asn	Leu	Gln	Ala	Ala	Ser	Ser	Gln	Gly	Gly	Gly	Tyr	Asp	Met
	290					295					300				
Arg	Arg	Leu	Leu	Asp	Gly	Thr	Val	Val	Ser	Arg	His	Pro	Glu	Lys	Ala
305					310					315					320
Val	Thr	Phe	Val	Glu	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu
			325						330					335	
Ser	Thr	Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu
		340						345					350		

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
 355 360 365

Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
 370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
 385 390 395 400

Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
 405 410 415

Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430

Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
 435 440 445

Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
 450 455 460

Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
 465 470 475 480

Val Gln Lys

<210> 11
 <211> 1458
 <212> DNA
 <213> Bacillus sp.

<220>
 <221> CDS
 <222> (1)..(1458)
 <223> AA560

<400> 11
 cac cat aat ggt acg aac ggc aca atg atg cag tac ttt gaa tgg tat 48
 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
 1 5 10 15

cta cca aat gac gga aac cat tgg aat aga tta agg tct gat gca agt 96
 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Ser Asp Ala Ser
 20 25 30

aac cta aaa gat aaa ggg atc tca gcg gtt tgg att cct cct gca tgg Asn Leu Lys Asp Lys Gly Ile Ser Ala Val Trp Ile Pro Pro Ala Trp 35 40 45	144
aag ggt gcc tct caa aat gat gtg ggg tat ggt gct tat gat ctg tat Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr 50 55 60	192
gat tta gga gaa ttc aat caa aaa gga acc att cgt aca aaa tat gga Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly 65 70 75 80	240
acg cgc aat cag tta caa gct gca gtt aac gcc ttg aaa agt aat gga Thr Arg Asn Gln Leu Gln Ala Ala Val Asn Ala Leu Lys Ser Asn Gly 85 90 95	288
att caa gtg tat ggc gat gtt gta atg aat cat aaa ggg gga gca gac Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp 100 105 110	336
gct acc gaa atg gtt agg gca gtt gaa gta aac ccg aat aat aga aat Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn 115 120 125	384
caa gaa gtg tcc ggt gaa tat aca att gag gct tgg aca aag ttt gac Gln Glu Val Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp 130 135 140	432
ttt cca gga cga ggt aat act cat tca aac ttc aaa tgg aga tgg tat Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr 145 150 155 160	480
cac ttt gat gga gta gat tgg gat cag tca cgt aag ctg aac aat cga His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Lys Leu Asn Asn Arg 165 170 175	528
att tat aaa ttt aga ggt gat gga aaa ggg tgg gat tgg gaa gtc gat Ile Tyr Lys Phe Arg Gly Asp Gly Lys Gly Trp Asp Trp Glu Val Asp 180 185 190	576
aca gaa aac ggt aac tat gat tac cta atg tat gca gat att gac atg Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met 195 200 205	624
gat cac cca gag gta gtg aat gag cta aga aat tgg ggt gtt tgg tat Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr 210 215 220	672
acg aat aca tta ggc ctt gat ggt ttt aga ata gat gca gta aaa cat Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His 225 230 235 240	720
ata aaa tac agc ttt act cgt gat tgg att aat cat gtt aga agt gca Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala 245 250 255	768

act ggc aaa aat atg ttt gcg gtt gcg gaa ttt tgg aaa aat gat tta	816
Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu	
260 265 270	
ggt gct att gaa aac tat tta aac aaa aca aac tgg aac cat tca gtc	864
Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val	
275 280 285	
ttt gat gtt ccg ctg cac tat aac ctc tat aat gct tca aaa agc gga	912
Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly	
290 295 300	
ggg aat tat gat atg agg caa ata ttt aat ggt aca gtc gtg caa aga	960
Gly Asn Tyr Asp Met Arg Gln Ile Phe Asn Gly Thr Val Val Gln Arg	
305 310 315 320	
cat cca atg cat gct gtt aca ttt gtt gat aat cat gat tcg caa cct	1008
His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro	
325 330 335	
gaa gaa gct tta gag tct ttt gtt gaa gaa tgg ttc aaa cca tta gcg	1056
Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala	
340 345 350	
tat gct ttg aca tta aca cgt gaa caa ggc tac cct tct gta ttt tat	1104
Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr	
355 360 365	
gga gat tat tat ggc att cca acg cat ggt gta cca gcg atg aaa tcg	1152
Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser	
370 375 380	
aaa att gac ccg att cta gaa gcg cgt caa aag tat gca tat gga aga	1200
Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Arg	
385 390 395 400	
caa aat gac tac tta gac cat cat aat atc atc ggt tgg aca cgt gaa	1248
Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu	
405 410 415	
ggg aat aca gca cac ccc aac tcc ggt tta gct act atc atg tcc gat	1296
Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp	
420 425 430	
ggg gca gga gga aat aag tgg atg ttt gtt ggg cgt aat aaa gct ggt	1344
Gly Ala Gly Gly Asn Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly	
435 440 445	
caa gtt tgg acc gat atc act gga aat cgt gca ggt act gtt acg att	1392
Gln Val Trp Thr Asp Ile Thr Gly Asn Arg Ala Gly Thr Val Thr Ile	
450 455 460	
aat gct gat gga tgg ggt aat ttt tct gta aat gga gga tca gtt tct	1440
Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser	
465 470 475 480	
att tgg gta aac aaa taa	1458

Ile Trp Val Asn Lys
485

<210> 12
<211> 485
<212> PRT
<213> Bacillus sp.

<400> 12

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Ser Asp Ala Ser
20 25 30

Asn Leu Lys Asp Lys Gly Ile Ser Ala Val Trp Ile Pro Pro Ala Trp
35 40 45

Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly
65 70 75 80

Thr Arg Asn Gln Leu Gln Ala Ala Val Asn Ala Leu Lys Ser Asn Gly
85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn
115 120 125

Gln Glu Val Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Lys Leu Asn Asn Arg
165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Gly Trp Asp Trp Glu Val Asp
180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met
 195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
 210 215 220

Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
 225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala
 245 250 255

Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
 260 265 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
 275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly
 290 295 300

Gly Asn Tyr Asp Met Arg Gln Ile Phe Asn Gly Thr Val Val Gln Arg
 305 310 315 320

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
 325 330 335

Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala
 340 345 350

Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
 355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
 370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Arg
 385 390 395 400

Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
 405 410 415

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Ala Gly Gly Asn Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
435 440 445

Gln Val Trp Thr Asp Ile Thr Gly Asn Arg Ala Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Ile Trp Val Asn Lys
485

<210> 13
<211> 485
<212> PRT
<213> bacillus sp. 707

<400> 13

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Asn Ser Asp Ala Ser
20 25 30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
35 40 45

Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

Thr Arg Ser Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn

115		120		125
Gln Glu Val Thr Gly Glu Tyr Thr Ile Glu Ala Trp Thr Arg Phe Asp				
130		135		140
Phe Pro Gly Arg Gly Asn Thr His Ser Ser Phe Lys Trp Arg Trp Tyr				
145		150		155
				160
His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Arg Leu Asn Asn Arg				
	165		170	175
Ile Tyr Lys Phe Arg Gly His Gly Lys Ala Trp Asp Trp Glu Val Asp				
	180		185	190
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met				
	195		200	205
Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr				
	210		215	220
Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His				
225		230		235
				240
Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala				
	245		250	255
Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu				
	260		265	270
Gly Ala Ile Glu Asn Tyr Leu Gln Lys Thr Asn Trp Asn His Ser Val				
	275		280	285
Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly				
	290		295	300
Gly Asn Tyr Asp Met Arg Asn Ile Phe Asn Gly Thr Val Val Gln Arg				
305		310		315
				320
His Pro Ser His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro				
	325		330	335
Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala				
	340		345	350

Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
 355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Arg Ser
 370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Lys
 385 390 395 400

Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
 405 410 415

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
 420 425 430

Gly Ala Gly Gly Ser Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
 435 440 445

Gln Val Trp Ser Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
 450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
 465 470 475 480

Ile Trp Val Asn Lys
 485

<210> 14
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 14
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<210> 15
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 15
gaatttgtag atacgatttt g 21

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
cgattgctga cgctgttatt tgcg 24

<210> 17
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
cttgttccct tgcagaacc aatg 24

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
gtcatagttg ccgaaatctg tatcgacttc 30

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
gacctgcagt caggcaacta 20

<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 20

tagagtcgac ctgcagggcat

20

09/9257 p

Bacillus sp. yQ catcataatg gaacaaatgg tactatgatg caatatttcg
aatggatatt gccaaatgac 60
gggaatcatt ggaacagggt gagggatgac gcagctaact taaagagtaa agggataaca
120
gctgtatgga tcccacctgc atggaagggg acttcccaga atgatgtagg ttatggagcc
180
tatgatttat atgatcttgg agagtttaac cagaagggga cgttcgtac aaaatatgga
240
acacgcaacc agctacaggc tgcggtgacc tctttaaaaa ataacggcat tcaggatat
300
ggtgatgtcg tcatgaatca taaaggtgga gcagatggta cggaaattgt aaatgcggta
360
gaagtgaatc ggagcaaccg aaaccaggaa acctcaggag agtatgcaat agaagcgtgg
420
acaaagtttg attttcctgg aagaggaaat aaccattcca gctttaagtg gcgctggtat
480